

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1.-101. (Canceled)

102. (New) A method for separating a nucleic acid molecule of interest with one parental origin from a nearly identical nucleic acid molecule with the other parental origin in a population of nucleic acid molecules, the method comprising:

(a) providing a population of nucleic acid molecules isolated from a biological sample, wherein

(1) the population of nucleic acid molecules comprises (i) a nucleic acid molecule of interest, and (ii) another nucleic acid molecule that is nearly identical to the nucleic acid molecule of interest but with the other parental origin,

(2) one strand of the nucleic acid molecule of interest comprises (i) a target nucleic acid sequence, and (ii) a distinguishing element, and

(3) the distinguishing element distinguishes the nucleic acid molecule of interest from the other nucleic acid molecule that is nearly identical to the nucleic acid molecule of interest but with the other parental origin;

(b) contacting the population of nucleic acid molecules with a targeting element, wherein the targeting element comprises an oligonucleotide that (i) binds specifically to the target nucleic acid sequence of the nucleic acid molecule of interest in the population of nucleic acid molecules, and (ii) overlaps the distinguishing element of the nucleic acid molecule of interest at or near the 3'-end of the oligonucleotide;

(c) selectively attaching a separation group to the targeting element bound to the target nucleic acid sequence in the presence of a polymerase, wherein (i) the attachment of

the separation group to the targeting element occurs only if the targeting element is bound to the target nucleic acid sequence of the nucleic acid molecule of interest, but not if the targeting element is bound to the other nucleic acid molecule that is nearly identical to the nucleic acid molecule of interest but with the other parental origin, and (ii) the separation group comprises an immobilizable and non-terminating nucleotide;

(d) immobilizing the nucleic acid molecule of interest and the bound oligonucleotide via the attached separation group to a substrate, thereby forming an immobilized targeting element-separation group complex to which the nucleic acid molecule of interest is bound; and

(e) removing the immobilized targeting element-separation group complex from the population of nucleic acid molecules, thereby separating the nucleic acid molecule of interest bound to the immobilized oligonucleotide-separation group complex from the other nucleic acid molecule that is nearly identical to the nucleic acid molecule of interest but with the other parental origin in the population of nucleic acid molecules.

103. (New) The method of claim 102, wherein the population of nucleic acid molecules is a population of genomic DNA molecules.

104. (New) The method of claim 102, wherein the population of nucleic acid molecules is a population of RNA molecules.

105. (New) The method of claim 102, wherein the immobilizable and non-terminating nucleotide is a fluorescein-modified deoxynucleotide triphosphate.

106. (New) The method of claim 102, wherein the immobilizable and non-terminating nucleotide is a biotinylated deoxynucleotide triphosphate.

107. (New) The method of claim 102, wherein the extension product comprises multiple separation groups.

108. (New) The method of claim 107, wherein the extension product is immobilized to the substrate via the multiple separation groups.

109. (New) The method of claim 108, wherein the nucleic acid molecule of interest is topologically attached to the substrate via the extension product.

110. (New) The method of claim 109 further comprising washing the nucleic acid molecule of interest topologically attached to the substrate at high stringency.

111. (New) The method of claim 102, wherein the distinguishing element is a heterozygous single nucleotide polymorphism.

112. (New) The method of claim 111, wherein the 3' terminus of the oligonucleotide is complementary to the heterozygous single nucleotide polymorphism.

113. (New) The method of claim 102 further comprising (f) characterizing the nucleic acid molecule of interest separated from the other nucleic acid molecule that is nearly identical to the nucleic acid molecule of interest but with the other parental origin in the population of nucleic acid molecules.

114. (New) The method of claim 113, wherein the population of nucleic acid molecules is a population of genomic DNA molecules, and wherein step (f) comprises characterizing sites in the nucleic acid molecule of interest that constitute a haplotype.

115. (New) The method of claim 102, wherein the substrate is a particle, bead, magnetic bead, or glass surface, or plastic.

116. (New) The method of claim 102, wherein the separation group or the targeting element comprises a cleavable linker.

117. (New) The method of claim 102, wherein step (d) is performed with relative motion between the bound oligonucleotide and the substrate to achieve selectivity and efficiency in forming the immobilized oligonucleotide-separation group complex.

118. (New) The method of claim 102, wherein the population of nucleic acid molecule is a population of genomic DNA molecules and wherein prior to step (b), the genomic DNA molecules are denatured with NaOH or by heat.

119. (New) The method of claim 102, wherein the population of nucleic acid molecules is a population of genomic DNA molecules, and the oligonucleotide is coated with a DNA-binding protein.

120. (New) The method of claim 119, wherein the DNA binding protein is RecA.

121. (New) The method of claim 102, wherein the nucleic acid molecule of interest is more than 100 Kbp in length.

122. (New) The method of claim 102, wherein steps (a) to (e) are performed in an automated high-throughput format.

123. (New) The method of claim 102, wherein steps (a) to (e) are performed in a miniaturized and integrated format.

124. (New) The method of claim 102, further comprising contacting the population of nucleic acid molecules with a second targeting element, wherein

the population of nucleic acid molecules comprises a second nucleic acid molecule of interest,

the second nucleic acid molecule of interest comprises (i) a second target nucleic acid sequence and (ii) a second distinguishing element,

the second distinguishing element distinguishes the second nucleic acid molecule of interest from another nucleic acid molecule that is nearly identical to the second nucleic acid molecule of interest, but from a parental origin different from that of the second nucleic acid molecule of interest, and

the second targeting element comprises a second oligonucleotide that (i) binds specifically to the second target nucleic acid sequence of the second nucleic acid molecule of interest in the population of nucleic acid molecules, and (ii) overlaps the second distinguishing element of the second nucleic acid molecule of interest at or near the 3'-end of the second oligonucleotide;

selectively attaching a second separation group to the second targeting element bound to the second target nucleic acid sequence in the presence of the polymerase, wherein the attachment of the second separation group to the second targeting element occurs only if the second targeting element is bound to the second target nucleic acid sequence of the second nucleic acid molecule of interest, but not if the second targeting element is bound to the other second nucleic acid molecule that is nearly identical to the second nucleic acid molecule of interest but with a different parental origin, and (ii) the second separation group comprises a second immobilizable and non-terminating nucleotide;

immobilizing the second nucleic acid molecule of interest and the bound second targeting element via the attached second separation group to a second substrate, thereby forming an immobilized second targeting element-second separation group complex to which the second nucleic acid molecule of interest is bound; and

removing the immobilized second targeting element-second separation group complex from the population of nucleic acid molecules, thereby separating the second nucleic acid molecule of interest bound to the immobilized second targeting element-second separation group complex from the other second nucleic acid molecule that is nearly identical to the second nucleic acid molecule of interest but with a different parental origin in the population of nucleic acid molecules.